



0400
5-7-01

RAW SEQUENCE LISTING **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/828,995
Source: O/PE
Date Processed by STIC: 4/30/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/828,995

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 _____ Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 _____ Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 _____ Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 _____ Misaligned Amino Acid The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
Numbering between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 _____ Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 _____ Variable Length Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.
- 7 _____ PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. **This applies primarily to the mandatory <220>-<223>
sections for Artificial or Unknown sequences.**
- 8 _____ Skipped Sequences Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(OLD RULES) **(2) INFORMATION FOR SEQ ID NO:X:**
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 _____ Skipped Sequences Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
(NEW RULES) **<210> sequence id number**
<400> sequence id number
000
- 10 _____ Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES) Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 _____ Use of "Artificial" Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules.
(NEW RULES) Valid response is Artificial Sequence.
- 12 _____ Use of <220>Feature Sequence(s) _____ are missing the <220>Feature and associated headings.
(NEW RULES) Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial Sequence" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 _____ PatentIn ver. 2.0 "bug" **Please do not use "Copy to Disk" function of PatentIn version 2.0.** This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

O.I.P.E.

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/828,995

DATE: 04/30/2001

TIME: 09:06:25

Input Set : A:\A1-71.app

Output Set: N:\CRF3\04302001\I828995.raw

Does Not Comply
Corrected Diskette Needed

3 <110> APPLICANT: McCall, Catherine A.
 4 Tang, Liang
 5 Heska Corporation
 7 <120> TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATED TO CANINE IgG AND
 8 CANINE IL-13 RECEPTORS
 10 <130> FILE REFERENCE: AL-7
 OK-> 12 <140> CURRENT APPLICATION NUMBER: US/09/828,995
 13 <141> CURRENT FILING DATE: 2001-04-09
 15 <150> PRIOR APPLICATION NUMBER: 60/195,659
 16 <151> PRIOR FILING DATE: 2000-04-07
 18 <150> PRIOR APPLICATION NUMBER: 60/195,874
 19 <151> PRIOR FILING DATE: 2000-04-07
 21 <160> NUMBER OF SEQ ID NOS: 104
 23 <170> SOFTWARE: PatentIn Ver. 2.1

ERRORED SEQUENCES

2874 <210> SEQ ID NO: 59
 2875 <211> LENGTH: 878
 2876 <212> TYPE: DNA
 2877 <213> ORGANISM: Canis familiaris
 2879 <400> SEQUENCE: 59
 E--> 2880 tttttttttt tttttttt taaaataaga tttattcaat atttgaggaa aagcttcagt 60
 2881 ttaataagac tcatatttaa catctggcca taagactgaa agttactgag tcaacagaat 120
 2882 gtgtcttgat gagaaaagac ttcttttttt gtatgaaaga tcgttttcag taaagccctt 180
 2883 tgcttataca aaagcaggca agttattacc aaaacaaata ttgagacaaa agcaaatggt 240
 2884 atcaagaaaa atactaagggt ttcttccat atgtcacctt tccagcattg ttcactcactc 300
 2885 cactcactcc agattccatc atctgagcaa taaatattca ctttacttct taccaaaaag 360
 2886 cataattttt ggctttcatt tgatgttctt gtgatttgta tctcattctc aactgtggta 420
 2887 gtcacccaag tagtaccatc ctctgtgaat tcaatttcat aaatgaaaca tttggctgga 480
 2888 atgggtcctt taggcatgtt ccatttcagg ttaatttcct ctgaattcct cacagtaaga 540
 2889 ctaaggtagt ctggtggcat aggtttaact atattttgaa gctgaaaaat aaaatagctg 600
 2890 ggtctgatag gctgggattc tgatgaccca ttaacacaga tgtagaaatc tttatagtct 660
 2891 gatgactcca aatagggaaa cctgcacccc atattttttc cattaacctt gatgtaatca 720
 2892 gtacactctg ctgaatggc caagccctca taccagtaaa acaactggta attgggatca 780
 2893 aaatggacac ccatgccagg tttccaagag cagactaaat attgccagtt gtaatataca 840
 2894 cagtccatat cttgaatttt agtttcccga tttccttg 878

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/828,995

DATE: 04/30/2001

TIME: 09:06:27

Input Set : A:\A1-71.app

Output Set: N:\CRF3\04302001\I828995.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application Number
L:701 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:956 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:18
L:956 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:18
L:956 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:1317 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
L:1318 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
L:1326 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
L:1386 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:26
L:1386 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:26
L:1386 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:26
L:1386 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26
L:1389 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:26
L:1389 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:26
L:1389 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:26
L:1389 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26
L:1422 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:27
L:1422 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:27
L:1422 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
L:1482 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:1484 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:1534 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:30
L:1534 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:30
L:1534 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30
L:1535 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:30
L:1535 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:30
L:1535 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30
L:2204 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:40
L:2204 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:40
L:2204 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40
L:2314 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:48
L:2314 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:48
L:2314 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:48
L:2814 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:57
L:2880 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:59
L:3016 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:60
L:3114 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:62
L:3114 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:62
L:3114 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:62
L:4829 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:83
L:4829 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:83
L:4829 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:83
L:4845 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:84
L:4845 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:84
L:4845 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:84
L:4861 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:85
L:4861 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:85
L:4861 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:85

VERIFICATION SUMMARY

DATE: 04/30/2001

PATENT APPLICATION: US/09/828,995

TIME: 09:06:27

Input Set : A:\A1-71.app

Output Set: N:\CRF3\04302001\I828995.raw

L:4877 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:86
L:4877 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:86
L:4877 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:86
L:4893 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:87
L:4893 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:87
L:4893 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:87
L:4909 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:88
L:4909 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:88
L:4909 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:88